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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 348 base pairs
5 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

15 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 14..325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

20	GGAATTCTTA ATA ATG TCC GTA CAA GAA ACC ATC TCC CCA GGA GAC Met Ser Val Gln Val Glu Thr Ile Ser Pro Gly Asp 1 5 10	49
25	GGG CGC ACC TTC CCC AAG CGC GGC CAG ACC TGC GTG GTG CAC TAC ACC Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr 15 20 25	97
30	GGG ATG CTT GAA GAT GGA AAG AAA TTT GAT TCC TCC CGT GAC CGT AAC Gly Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn 30 35 40	145
35	AAG CCC TTT AAG TTT ATG CTA GGC AAG CAG GAG GTG ATC CGA GGC TGG Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp 45 50 55 60	193
40	GAA GAA GGG GTT GCC CAG ATG AGT GTG GGT CAG CGT GCC AAA CTG ACT Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr 65 70 75	241
45	ATA TCT CCA GAT TAT GCC TAT GGT GCC ACT GGG CAC CCA GGC ATC ATC Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile 80 85 90	289
	CCA CCA CAT GCC ACT CTC GTC TTC GAT GTG GAG CTT CTAAAACTGG Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu 95 100	335
	AATGACGGGA TCC	348

50

(2) INFORMATION FOR SEQ ID NO:2:

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7943 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: cDNA

65 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 80..7726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

70 ACGGGGCCTG AAGCGCGGT ACCGGTGCTG GCGGCGGCAG CTGAGGCCTT GGCGAAGCC 60

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	GC GCGAACCT CAGGGCAAG ATG CTT GGA ACC GGA CCT GCC GCC ACC ACC	112
	Met Leu Gly Thr Gly Pro Ala Ala Ala Thr Thr	
	1 5 10	
5	GCT GCC ACC ACA TCT AGC AAT GTG AGC GTC CTG CAG CAG TTT GCC AGT Ala Ala Thr Thr Ser Ser Asn Val Ser Val Leu Gln Gln Phe Ala Ser	160
	15 20 25	
10	GGC CTA AAG AGC CGG AAT GAG GAA ACC AGG GCC AAA GCC GCC AAG GAG Gly Leu Lys Ser Arg Asn Glu Glu Thr Arg Ala Lys Ala Ala Lys Glu	208
	30 35 40	
15	CTC CAG CAC TAT GTC ACC ATG GAA CTC CGA GAG ATG AGT CAA GAG GAG Leu Gln His Tyr Val Thr Met Glu Leu Arg Glu Met Ser Gln Glu Glu	256
	45 50 55	
20	TCT ACT CGC TTC TAT GAC CAA CTG AAC CAT CAC ATT TTT GAA TTG GTT Ser Thr Arg Phe Tyr Asp Gln Leu Asn His His Ile Phe Glu Leu Val	304
	60 65 70 75	
25	TCC AGC TCA GAT GCC AAT GAG AGG AAA GGT GGC ATC TTG GCC ATA GCT Ser Ser Ser Asp Ala Asn Glu Arg Lys Gly Gly Ile Leu Ala Ile Ala	352
	80 85 90	
30	AGC CTC ATA GGA GTG GAA GGT GGG AAT GCC ACC CGA ATT GGC AGA TTT Ser Leu Ile Gly Val Glu Gly Gly Asn Ala Thr Arg Ile Gly Arg Phe	400
	95 100 105	
35	GCC AAC TAT CTT CGG AAC CTC CTC CCC TCC AAT GAC CCA GTT GTC ATG Ala Asn Tyr Leu Arg Asn Leu Leu Pro Ser Asn Asp Pro Val Val Met	448
	110 115 120	
40	GAA ATG GCA TCC AAG GCC ATT GGC CGT CTT GCC ATG GCA GGG GAC ACT Glu Met Ala Ser Lys Ala Ile Gly Arg Leu Ala Met Ala Gly Asp Thr	496
	125 130 135	
45	TTT ACC GCT GAG TAC GTG GAA TTT GAG GTG AAG CGA GCC CTG GAA TGG Phe Thr Ala Glu Tyr Val Glu Phe Glu Val Lys Arg Ala Leu Glu Trp	544
	140 145 150 155	
50	CTG GGT GCT GAC CGC AAT GAG GGC CGG AGA CAT GCA GCT GTC CTG GTT Leu Gly Ala Asp Arg Asn Glu Gly Arg Arg His Ala Ala Val Leu Val	592
	160 165 170	
55	CTC CGT GAG CTG GCC ATC AGC GTC CCT ACC TTC TTC TTC CAG CAA GTG Leu Arg Glu Leu Ala Ile Ser Val Pro Thr Phe Phe Phe Gln Gln Val	640
	175 180 185	
60	CAA CCC TTC TTT GAC AAC ATT TTT GTG GCC GTG TGG GAC CCC AAA CAG Gln Pro Phe Phe Asp Asn Ile Phe Val Ala Val Trp Asp Pro Lys Gln	688
	190 195 200	
65	GCC ATC CGT GAG GGA GCT GTA GCC GCC CTT CGT GCC TGT CTG ATT CTC Ala Ile Arg Glu Gly Ala Val Ala Ala Leu Arg Ala Cys Leu Ile Leu	736
	205 210 215	
70	ACA ACC CAG CGT GAG CCG AAG GAG ATG CAG AAG CCT CAG TGG TAC AGG Thr Thr Gln Arg Glu Pro Lys Glu Met Gln Lys Pro Gln Trp Tyr Arg	784
	220 225 230 235	
75	CAC ACA TTT GAA GAA GCA GAG AAG GGA TTT GAT GAG ACC TTG GCC AAA His Thr Phe Glu Glu Ala Glu Lys Gly Phe Asp Glu Thr Leu Ala Lys	832
	240 245 250	
80	GAG AAG GGC ATG AAT CGG GAT GAT CGG ATC CAT GGA GCC TTG TTG ATC Glu Lys Gly Met Asn Arg Asp Asp Arg Ile His Gly Ala Leu Leu Ile	880
	255 260 265	
85	CTT AAC GAG CTG GTC CGA ATC AGC AGC ATG GAG GGA GAG CGT CTG AGA Leu Asn Glu Leu Val Arg Ile Ser Ser Met Glu Gly Glu Arg Leu Arg	928
	270 275 280	

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	GAA GAA ATG GAA GAA ATC ACA CAG CAG CAG CTG GTA CAC GAC AAG TAC Glu Glu Met Glu Glu Ile Thr Gln Gln Gln Leu Val His Asp Lys Tyr 285 290 295	976
5	TGC AAA GAT CTC ATG GGC TTC GGA ACA AAA CCT CGT CAC ATT ACC CCC Cys Lys Asp Leu Met Gly Phe Gly Thr Lys Pro Arg His Ile Thr Pro 300 305 310 315	1024
10	TTC ACC AGT TTC CAG GCT GTA CAG CCC CAG CAG TCA AAT GCC TTG GTG Phe Thr Ser Phe Gln Ala Val Gln Pro Gln Gln Ser Asn Ala Leu Val 320 325 330	1072
15	GGG CTG CTG GGG TAC AGC TCT CAC CAA GGC CTC ATG GGA TTT GGG ACC Gly Leu Leu Gly Tyr Ser Ser His Gln Gly Leu Met Gly Phe Gly Thr 335 340 345	1120
20	TCC CCC AGT CCA GCT AAG TCC ACC CTG GTG GAG AGC CGG TGT TGC AGA Ser Pro Ser Pro Ala Lys Ser Thr Leu Val Glu Ser Arg Cys Cys Arg 350 355 360	1168
25	GAC TTG ATG GAG GAG AAA TTT GAT CAG GTG TGC CAG TGG GTG CTG AAA Asp Leu Met Glu Glu Lys Phe Asp Gln Val Cys Gln Trp Val Leu Lys 365 370 375	1216
30	TGC AGG AAT AGC AAG AAC TCG CTG ATC CAA ATG ACA ATC CTT AAT TTG Cys Arg Asn Ser Lys Asn Ser Leu Ile Gln Met Thr Ile Leu Asn Leu 380 385 390 395	1264
35	TTG CCC CGC TTG GCT GCA TTC CGA CCT TCT GCC TTC ACA GAT ACC CAG Leu Pro Arg Leu Ala Ala Phe Arg Pro Ser Ala Phe Thr Asp Thr Gln 400 405 410	1312
40	TAT CTC CAA GAT ACC ATG AAC CAT GTC CTA AGC TGT GTC AAG AAG GAG Tyr Leu Gln Asp Thr Met Asn His Val Leu Ser Cys Val Lys Lys Glu 415 420 425	1360
45	AAG GAA CGT ACA GCG GCC TTC CAA GCC CTG GGG CTA CTT TCT GTG GCT Lys Glu Arg Thr Ala Ala Phe Gln Ala Leu Gly Leu Leu Ser Val Ala 430 435 440	1408
50	GTG AGG TCT GAG TTT AAG GTC TAT TTG CCT CGC GTG CTG GAC ATC ATC Val Arg Ser Glu Phe Lys Val Tyr Leu Pro Arg Val Leu Asp Ile Ile 445 450 455	1456
55	CGA GCG GCC CTG CCC CCA AAG GAC TTC GCC CAT AAG AGG CAG AAG GCA Arg Ala Ala Leu Pro Pro Lys Asp Phe Ala His Lys Arg Gln Lys Ala 460 465 470 475	1504
60	ATG CAG GTG GAC GCC ACA GTC TTC ACT TGC ATC AGC ATG CTG GCT CGA Met Gln Val Asp Ala Thr Val Phe Thr Cys Ile Ser Met Leu Ala Arg 480 485 490	1552
65	GCA ATG GGG CCA GCC ATC CAG CAG GAT ATC AAG GAG CTG CTG GAG CCC Ala Met Gly Pro Gly Ile Gln Gln Asp Ile Lys Glu Leu Leu Glu Pro 495 500 505	1600
70	ATG CTG GCA GTG GGA CTA AGC CCT GCC CTC ACT GCA GTG CTC TAC GAC Met Leu Ala Val Gly Leu Ser Pro Ala Leu Thr Ala Val Leu Tyr Asp 510 515 520	1648
75	CTG AGC CGT CAG ATT CCA CAG CTA AAG AAG GAC ATT CAA GAT GGG CTA Leu Ser Arg Gln Ile Pro Gln Leu Lys Lys Asp Ile Gln Asp Gly Leu 525 530 535	1696
80	CTG AAA ATG CTG TCC CTG GTC CTT ATG CAC AAA CCC CTT CGC CAC CCA Leu Lys Met Leu Ser Leu Val Leu Met His Lys Pro Leu Arg His Pro 540 545 550 555	1744
85	GGC ATG CCC AAG GGC CTG GCC CAT CAG CTG GCC TCT CCT GGC CTC ACG Gly Met Pro Lys Gly Leu Ala His Gln Leu Ala Ser Pro Gly Leu Thr	1792

560

565

570

5	ACC CTC CCT GAG GCC AGC GAT GTG GGC AGC ATC ACT CTT GCC CTC CGA Thr Leu Pro Glu Ala Ser Asp Val Gly Ser Ile Thr Leu Ala Leu Arg 575	580	585	1840	
10	ACG CTT GGC AGC TTT GAA TTT GAA GGC CAC TCT CTG ACC CAA TTT GTT Thr Leu Gly Ser Phe Glu Phe Gly His Ser Leu Thr Gln Phe Val 590	595	600	1888	
15	CGC CAC TGT GCG GAT CAT TTC CTG AAC AGT GAG CAC AAG GAG ATC CGC Arg His Cys Ala Asp His Phe Leu Asn Ser Glu His Lys Glu Ile Arg 605	610	615	1936	
20	ATG GAG GCT GCC CGC ACC TGC TCC CGC CTG CTC ACA CCC TCC ATC CAC Met Glu Ala Ala Arg Thr Cys Ser Arg Leu Leu Thr Pro Ser Ile His 620	625	630	1984	
25	CTC ATC AGT GGC CAT GCT CAT GTG GTT AGC CAG ACC GCA GTG CAA GTG Leu Ile Ser Gly His Ala His Val Val Ser Gln Thr Ala Val Gln Val 640	645	650	2032	
30	GTG GCA GAT GTG CTT AGC AAA CTG CTC GTA GTT GGG ATA ACA GAT CCT Val Ala Asp Val Leu Ser Lys Leu Leu Val Val Gly Ile Thr Asp Pro 655	660	665	2080	
35	GAC CCT GAC ATT CGC TAC TGT GTC TTG GCG TCC CTG GAC GAG CGC TTT Asp Pro Asp Ile Arg Tyr Cys Val Leu Ala Ser Leu Asp Glu Arg Phe 670	675	680	2128	
40	GAT GCA CAC CTG GCC CAG GCG GAG AAC TTG CAG GCC TTG TTT GTG GCT Asp Ala His Leu Ala Gln Ala Glu Asn Leu Gln Ala Leu Phe Val Ala 685	690	695	2176	
45	CTG AAT GAC CAG GTG TTT GAG ATC CGG GAG CTG GCC ATC TGC ACT GTG Leu Asn Asp Gln Val Phe Glu Ile Arg Glu Leu Ala Ile Cys Thr Val 700	705	710	715	2224
50	GGC CGA CTC AGT AGC ATG AAC CCT GCC TTT GTC ATG CCT TTC CTG CGC Gly Arg Leu Ser Ser Met Asn Pro Ala Phe Val Met Pro Phe Leu Arg 720	725	730	2272	
55	AAG ATG CTC ATC CAG ATT TTG ACA GAG TTG GAG CAC AGT GGG ATT GGA Lys Met Leu Ile Gln Ile Leu Thr Glu Leu Glu His Ser Gly Ile Gly 735	740	745	2320	
60	AGA ATC AAA GAG CAG AGT GCC CGC ATG CTG GGG CAC CTG GTC TCC AAT Arg Ile Lys Glu Gln Ser Ala Arg Met Leu Gly His Leu Val Ser Asn 750	755	760	2368	
65	GCC CCC CGA CTC ATC CGC CCC TAC ATG GAG CCT ATT CTG AAG GCA TTA Ala Pro Arg Leu Ile Arg Pro Tyr Met Glu Pro Ile Leu Lys Ala Leu 765	770	775	2416	
70	ATT TTG AAA CTG AAA GAT CCA GAC CCT GAT CCA AAC CCA GGT GTG ATC Ile Leu Lys Leu Lys Asp Pro Asp Pro Asn Pro Gly Val Ile 780	785	790	795	2464
75	AAT AAT GTC CTG GCA ACA ATA GGA GAA TTG GCA CAG GTT AGT GGC CTG Asn Asn Val Leu Ala Thr Ile Gly Glu Leu Ala Gln Val Ser Gly Leu 800	805	810	2512	
80	GAA ATG AGG AAA TGG GTT GAT GAA CTT TTT ATT ATC ATC ATG GAC ATG Glu Met Arg Lys Trp Val Asp Glu Leu Phe Ile Ile Met Asp Met 815	820	825	2560	
85	CTC CAG GAT TCC TCT TTG TTG GCC AAA AGG CAG GTG GCT CTG TGG ACC Leu Gln Asp Ser Ser Leu Leu Ala Lys Arg Gln Val Ala Leu Trp Thr 830	835	840	2608	
90	CTG GGA CAG TTG GTG GCC AGC ACT GGC TAT GTA GAG CCC TAC AGG			2656	

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	Leu	Gly	Gln	Leu	Val	Ala	Ser	Thr	Gly	Tyr	Val	Val	Glu	Pro	Tyr	Arg	
	845						850					855					
5	AAG	TAC	CCT	ACT	TTG	CTT	GAG	GTG	CTA	CTG	AAT	TTT	CTG	AAG	ACT	GAG	2704
	Lys	Tyr	Pro	Thr	Leu	Leu	Glu	Val	Leu	Leu	Asn	Phe	Leu	Lys	Thr	Glu	
	860				865					870			875				
10	CAG	AAC	CAG	GGT	ACA	CGC	AGA	GAG	GCC	ATC	CGT	GTG	TTA	GGG	CTT	TTA	2752
	Gln	Asn	Gln	Gly	Thr	Arg	Arg	Glu	Ala	Ile	Arg	Val	Leu	Gly	Leu	Leu	
					880				885			890					
	GGG	GCT	TTG	GAT	CCT	TAC	AAG	CAC	AAA	GTG	AAC	ATT	GGC	ATG	ATA	GAC	2800
	Gly	Ala	Leu	Asp	Pro	Tyr	Lys	His	Lys	Val	Asn	Ile	Gly	Met	Ile	Asp	
					895				900			905					
15	CAG	TCC	CGG	GAT	GCC	TCT	GCT	GTC	AGC	CTG	TCA	GAA	TCC	AAG	TCA	AGT	2848
	Gln	Ser	Arg	Asp	Ala	Ser	Ala	Val	Ser	Leu	Ser	Glu	Ser	Lys	Ser	Ser	
					910				915			920					
20	CAG	GAT	TCC	TCT	GAC	TAT	AGC	ACT	AGT	GAA	ATG	CTG	GTC	AAC	ATG	GGA	2896
	Gln	Asp	Ser	Ser	Asp	Tyr	Ser	Thr	Ser	Glu	Met	Leu	Val	Asn	Met	Gly	
					925				930			935					
25	AAC	TTG	CCT	CTG	GAT	GAG	TTC	TAC	CCA	GCT	GTG	TCC	ATG	GTG	GCC	CTG	2944
	Asn	Leu	Pro	Leu	Asp	Glu	Phe	Tyr	Pro	Ala	Val	Ser	Met	Val	Ala	Leu	
					940				945			950			955		
30	ATG	CGG	ATC	TTC	CGA	GAC	CAG	TCA	CTC	TCT	CAT	CAT	CAC	ACC	ATG	GTT	2992
	Met	Arg	Ile	Phe	Arg	Asp	Gln	Ser	Leu	Ser	His	His	His	His	Thr	Met	Val
					960				965			970					
	GTC	CAG	GCC	ATC	ACC	TTC	ATC	TTC	AAG	TCC	CTG	GGA	CTC	AAA	TGT	GTG	3040
	Val	Gln	Ala	Ile	Thr	Phe	Ile	Phe	Lys	Ser	Leu	Gly	Leu	Lys	Cys	Val	
					975				980			985					
35	CAG	TTC	CTG	CCC	CAG	GTC	ATG	CCC	ACG	TTC	CTT	AAT	GTC	ATT	CGA	GTC	3088
	Gln	Phe	Leu	Pro	Gln	Val	Met	Pro	Thr	Phe	Leu	Asn	Val	Ile	Arg	Val	
					990				995			1000					
40	TGT	GAT	GGG	GCC	ATC	CGG	GAA	TTT	TTG	TTC	CAG	CAG	CTG	GGA	ATG	TTG	3136
	Cys	Asp	Gly	Ala	Ile	Arg	Glu	Phe	Leu	Phe	Gln	Gln	Leu	Gly	Met	Leu	
					1005				1010			1015					
45	GTG	TCC	TTT	GTG	AAG	AGC	CAC	ATC	AGA	CCT	TAT	ATG	GAT	GAA	ATA	GTC	3184
	Val	Ser	Phe	Val	Lys	Ser	His	Ile	Arg	Pro	Tyr	Met	Asp	Glu	Ile	Val	
					1020				1025			1030			1035		
50	ACC	CTC	ATG	AGA	GAA	TTC	TGG	GTC	ATG	AAC	ACC	TCA	ATT	CAG	AGC	ACG	3232
	Thr	Leu	Met	Arg	Glu	Phe	Trp	Val	Met	Asn	Thr	Ser	Ile	Gln	Ser	Thr	
					1040				1045			1050					
	ATC	ATT	CTT	CTC	ATT	GAG	CAA	ATT	GTG	GTA	GCT	CTT	GGG	GGT	GAA	TTT	3280
	Ile	Ile	Leu	Ile	Glu	Gln	Ile	Val	Val	Ala	Leu	Gly	Gly	Glu	Phe		
					1055				1060			1065					
55	AAG	CTC	TAC	CTG	CCC	CAG	CTG	ATC	CCA	CAC	ATG	CTG	CGT	GTC	TTC	ATG	3328
	Lys	Leu	Tyr	Leu	Pro	Gln	Leu	Ile	Pro	His	Met	Leu	Arg	Val	Phe	Met	
					1070				1075			1080					
60	CAT	GAC	AAC	AGC	CCA	GGC	CGC	ATT	GTC	TCT	ATC	AAG	TTA	CTG	GCT	GCA	3376
	His	Asp	Asn	Ser	Pro	Gly	Arg	Ile	Val	Ser	Ile	Lys	Leu	Leu	Ala	Ala	
					1085				1090			1095					
65	ATC	CAG	CTG	TTT	GGC	GCC	AAC	CTG	GAT	GAC	TAC	CTG	CAT	TTA	CTG	CTG	3424
	Ile	Gln	Leu	Phe	Gly	Ala	Asn	Leu	Asp	Asp	Tyr	Leu	His	Leu	Leu	Leu	
					1100				1105			1110			1115		
70	CCT	CCT	ATT	GTT	AAG	TTG	TTT	GAT	GCC	CCT	GAA	GCT	CCA	CTG	CCA	TCT	3472
	Pro	Pro	Ile	Val	Lys	Leu	Phe	Asp	Ala	Pro	Glu	Ala	Pro	Leu	Pro	Ser	
					1120				1125			1130					

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	CGA AAG GCA GCG CTA GAG ACT GTG GAC CGC CTG ACG GAG TCC CTG GAT Arg Lys Ala Ala Leu Glu Thr Val Asp Arg Leu Thr Glu Ser Leu Asp 1135 1140 1145	3520
5	TTC ACT GAC TAT GCC TCC CGG ATC ATT CAC CCT ATT GTT CGA ACA CTG Phe Thr Asp Tyr Ala Ser Arg Ile Ile His Pro Ile Val Arg Thr Leu 1150 1155 1160	3568
10	GAC CAG AGC CCA GAA CTG CGC TCC ACA GCC ATG GAC ACG CTG TCT TCA Asp Gln Ser Pro Glu Leu Arg Ser Thr Ala Met Asp Thr Leu Ser Ser 1165 1170 1175	3616
15	CTT GTT TTT CAG CTG GGG AAG AAG TAC CAA ATT TTC ATT CCA ATG GTG Leu Val Phe Gln Leu Gly Lys Lys Tyr Gln Ile Phe Ile Pro Met Val 1180 1185 1190 1195	3664
20	AAT AAA GTT CTG GTG CGA CAC CGA ATC AAT CAT CAG CGC TAT GAT GTG Asn Lys Val Leu Val Arg His Arg Ile Asn His Gln Arg Tyr Asp Val 1200 1205 1210	3712
25	CTC ATC TGC AGA ATT GTC AAG GGA TAC ACA CTT GCT GAT GAA GAG GAG Leu Ile Cys Arg Ile Val Lys Gly Tyr Thr Leu Ala Asp Glu Glu Glu 1215 1220 1225	3760
30	GAT CCT TTG ATT TAC CAG CAT CGG ATG CTT AGG AGT GGC CAA GGG GAT Asp Pro Leu Ile Tyr Gln His Arg Met Leu Arg Ser Gly Gln Gly Asp 1230 1235 1240	3808
35	GCA TTG GCT AGT GGA CCA GTG GAA ACA GGA CCC ATG AAG AAA CTG CAC Ala Leu Ala Ser Gly Pro Val Glu Thr Gly Pro Met Lys Lys Leu His 1245 1250 1255	3856
40	GTC AGC ACC ATC AAC CTC CAA AAG GCC TGG GGC GCT GCC AGG AGG GTC Val Ser Thr Ile Asn Leu Gln Lys Ala Trp Gly Ala Ala Arg Arg Val 1260 1265 1270 1275	3904
45	TCC AAA GAT GAC TGG CTG GAA TGG CTG AGA CGG CTG AGC CTG GAG CTG Ser Lys Asp Asp Trp Leu Glu Trp Leu Arg Arg Leu Ser Leu Glu Leu 1280 1285 1290	3952
50	CTG AAG GAC TCA TCA TCG CCC TCC CTG CGC TCC TGC TGG GCC CTG GCA Leu Lys Asp Ser Ser Pro Ser Leu Arg Ser Cys Trp Ala Leu Ala 1295 1300 1305	4000
55	CAG GCC TAC AAC CCG ATG GCC AGG GAT CTC TTC AAT GCT GCA TTT GTG Gln Ala Tyr Asn Pro Met Ala Arg Asp Leu Phe Asn Ala Ala Phe Val 1310 1315 1320	4048
60	TCC TGC TGG TCT GAA CTG AAT GAA GAT CAA CAG GAT GAG CTC ATC AGA Ser Cys Trp Ser Glu Leu Asn Glu Asp Gln Gln Asp Glu Leu Ile Arg 1325 1330 1335	4096
65	AGC ATC GAG TTG GCC CTC ACC TCA CAA GAC ATC GCT GAA GTC ACA CAG Ser Ile Glu Leu Ala Leu Thr Ser Gln Asp Ile Ala Glu Val Thr Gln 1340 1345 1350 1355	4144
70	ACC CTC TTA AAC TTG GCT GAA TTC ATG GAA CAC AGT GAC AAG GGC CCC Thr Leu Leu Asn Leu Ala Glu Phe Met Glu His Ser Asp Lys Gly Pro 1360 1365 1370	4192
	CTG CCA CTG AGA GAT GAC AAT GGC ATT GTT CTG CTG GGT GAG AGA GCT Leu Pro Leu Arg Asp Asp Asn Gly Ile Val Leu Leu Gly Glu Arg Ala 1375 1380 1385	4240
	GCC AAG TGC CGA GCA TAT GCC AAA GCA CTA CAC TAC AAA GAA CTG GAG Ala Lys Cys Arg Ala Tyr Ala Lys Ala Leu His Tyr Lys Glu Leu Glu 1390 1395 1400	4288
	TTC CAG AAA GGC CCC ACC CCT GCC ATT CTA GAA TCT CTC ATC AGC ATT Phe Gln Lys Gly Pro Thr Pro Ala Ile Leu Glu Ser Leu Ile Ser Ile 1405 1410 1415	4336

	AAT AAT AAG CTA CAG CAG CCG GAG GCA GCG GCC GGA GTG TTA GAA TAT Asn Asn Lys Leu Gln Gln Pro Glu Ala Ala Ala Gly Val Leu Glu Tyr 1420 1425 1430 1435	4384
5	GCC ATG AAA CAC TTT GGA GAG CTG GAG ATC CAG GCT ACC TGG TAT GAG Ala Met Lys His Phe Gly Glu Leu Glu Ile Gln Ala Thr Trp Tyr Glu 1440 1445 1450	4432
10	AAA CTG CAC GAG TGG GAG GAT GCC CTT GTG GCC TAT GAC AAG AAA ATG Lys Leu His Glu Trp Glu Asp Ala Leu Val Ala Tyr Asp Lys Lys Met 1455 1460 1465	4480
15	GAC ACC AAC AAG GAC GAC CCA GAG CTG ATG CTG GCC CGC ATG CGC TGC Asp Thr Asn Lys Asp Asp Pro Glu Leu Met Leu Gly Arg Met Arg Cys 1470 1475 1480	4528
20	CTC GAG GCC TTG GGG GAA TGG GGT CAA CTC CAC CAG CAG TGC TGT GAA Leu Glu Ala Leu Gly Glu Trp Gly Gln Leu His Gln Gln Cys Cys Glu 1485 1490 1495	4576
25	AAG TGG ACC CTG GTT AAT GAT GAG ACC CAA GCC AAG ATG GCC CGG ATG Lys Trp Thr Leu Val Asn Asp Glu Thr Gln Ala Lys Met Ala Arg Met 1500 1505 1510 1515	4624
30	GCT GCT GCA GCT GCA TGG GGT TTA GGT CAG TGG GAC AGC ATG GAA GAA Ala Ala Ala Ala Ala Trp Gly Leu Gly Gln Trp Asp Ser Met Glu Glu 1520 1525 1530	4672
35	TAC ACC TGT ATG ATC CCT CGG GAC ACC CAT GAT GGG GCA TTT TAT AGA Tyr Thr Cys Met Ile Pro Arg Asp Thr His Asp Gly Ala Phe Tyr Arg 1535 1540 1545	4720
40	GCT GTG CTG GCA CTG CAT CAG GAC CTC TTC TCC TTG GCA CAA CAG TGC Ala Val Leu Ala Leu His Gln Asp Leu Phe Ser Leu Ala Gln Gln Cys 1550 1555 1560	4768
45	ATT GAC AAG GCC AGG GAC CTG CTG GAT GCT GAA TTA ACT GCA ATG GCA Ile Asp Lys Ala Arg Asp Leu Leu Asp Ala Glu Leu Thr Ala Met Ala 1565 1570 1575	4816
50	GGA GAG AGT TAC AGT CGG GCA TAT GGG GCC ATG GTT TCT TGC CAC ATG Gly Glu Ser Tyr Ser Arg Ala Tyr Gly Ala Met Val Ser Cys His Met 1580 1585 1590 1595	4864
55	CTG TCC GAG CTG GAG GAG GTT ATC CAG TAC AAA CTT GTC CCC GAG CGA Leu Ser Glu Leu Glu Val Ile Gln Tyr Lys Leu Val Pro Glu Arg 1600 1605 1610	4912
60	CGA GAG ATC ATC CGC CAG ATC TGG TGG GAG AGA CTG CAG GGC TGC CAG Arg Glu Ile Ile Arg Gln Ile Trp Trp Glu Arg Leu Gln Gly Cys Gln 1615 1620 1625	4960
65	CGT ATC GTA GAG GAC TGG CAG AAA ATC CTT ATG GTG CGG TCC CTT GTG Arg Ile Val Glu Asp Trp Gln Ile Leu Met Val Arg Ser Leu Val 1630 1635 1640	5008
70	GTC AGC CCT CAT GAA GAC ATG AGA ACC TGG CTC AAG TAT GCA AGC CTG Val Ser Pro His Glu Asp Met Arg Thr Trp Leu Lys Tyr Ala Ser Leu 1645 1650 1655	5056
	TGC GGC AAG AGT GGC AGG CTG GCT CTT GCT CAT AAA ACT TTA GTG TTG Cys Gly Lys Ser Gly Arg Leu Ala Leu Ala His Lys Thr Leu Val Leu 1660 1665 1670 1675	5104
	CTC CTG GGA GTT GAT CCG TCT CGG CAA CTT GAC CAT CCT CTG CCA ACA Leu Leu Gly Val Asp Pro Ser Arg Gln Leu Asp His Pro Leu Pro Thr 1680 1685 1690	5152
	GTT CAC CCT CAG GTG ACC TAT GCC TAC ATG AAA AAC ATG TGG AAG AGT Val His Pro Gln Val Thr Tyr Ala Tyr Met Lys Asn Met Trp Lys Ser	5200

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	1695	1700	1705	
5	GCC CGC AAG ATC GAT GCC TTC CAG CAC ATG CAG CAT TTT GTC CAG ACC Ala Arg Lys Ile Asp Ala Phe Gln His Met Gln His Phe Val Gln Thr 1710 1715 1720			5248
10	ATG CAG CAA CAG GCC CAG CAT GCC ATC GCT ACT GAG GAC CAG CAG CAT Met Gln Gln Ala Gln His Ala Ile Ala Thr Glu Asp Gln Gln His 1725 1730 1735			5296
15	AAG CAG GAA CTG CAC AAG CTC ATG GCC CGA TGC TTC CTG AAA CTT GGA Lys Gln Glu Leu His Lys Leu Met Ala Arg Cys Phe Leu Lys Leu Gly 1740 1745 1750 1755			5344
20	GAG TGG CAG CTG AAT CTA CAG GGC ATC AAT GAG AGC ACA ATC CCC AAA Glu Trp Gln Leu Asn Leu Gln Gly Ile Asn Glu Ser Thr Ile Pro Lys 1760 1765 1770			5392
25	GTG CTG CAG TAC TAC AGC GCC GCC ACA GAG CAC GAC CGC AGC TGG TAC Val Leu Gln Tyr Tyr Ser Ala Ala Thr Glu His Asp Arg Ser Trp Tyr 1775 1780 1785			5440
30	AAG GCC TGG CAT GCG TGG GCA GTG ATG AAC TTC GAA GCT GTG CTA CAC Lys Ala Trp His Ala Trp Ala Val Met Asn Phe Glu Ala Val Leu His 1790 1795 1800			5488
35	TAC AAA CAT CAG AAC CAA GCC CGC GAT GAG AAG AAG AAA CTG CGT CAT Tyr Lys His Gln Asn Gln Ala Arg Asp Glu Lys Lys Lys Leu Arg His 1805 1810 1815			5536
40	GCC AGC GGG GCC AAC ATC ACC AAC GCC ACC ACT GCC GCC ACC ACG GCC Ala Ser Gly Ala Asn Ile Thr Asn Ala Thr Thr Ala Ala Thr Thr Ala 1820 1825 1830 1835			5584
45	GCC ACT GCC ACC ACT GCC AGC ACC GAG GGC AGC AAC AGT GAG AGC Ala Thr Ala Thr Thr Ala Ser Thr Glu Gly Ser Asn Ser Glu Ser 1840 1845 1850			5632
50	GAG GCC GAG AGC ACC GAG AAC AGC CCC ACC CCA TCG CCG CTG CAG AAG Glu Ala Glu Ser Thr Glu Asn Ser Pro Thr Pro Ser Pro Leu Gln Lys 1855 1860 1865			5680
55	AAG GTC ACT GAG GAT CTG TCC AAA ACC CTC CTG ATG TAC ACG GTG CCT Lys Val Thr Glu Asp Leu Ser Lys Thr Leu Leu Met Tyr Thr Val Pro 1870 1875 1880			5728
60	GCC GTC CAG GGC TTC TTC CGT TCC ATC TCC TTG TCA CGA GGC AAC AAC Ala Val Gln Gly Phe Phe Arg Ser Ile Ser Leu Ser Arg Gly Asn Asn 1885 1890 1895			5776
65	CTC CAG GAT ACA CTC AGA GTT CTC ACC TTA TGG TTT GAT TAT GGT CAC Leu Gln Asp Thr Leu Arg Val Leu Thr Leu Trp Phe Asp Tyr Gly His 1900 1905 1910 1915			5824
70	TGG CCA GAT GTC AAT GAG GCC TTA GTG GAG GGG GTG AAA GCC ATC CAG Trp Pro Asp Val Asn Glu Ala Leu Val Glu Gly Val Lys Ala Ile Gln 1920 1925 1930			5872
75	ATT GAT ACC TGG CTA CAG GTT ATA CCT CAG CTC ATT GCA AGA ATT GAT Ile Asp Thr Trp Leu Gln Val Ile Pro Gln Leu Ile Ala Arg Ile Asp 1935 1940 1945			5920
80	ACG CCC AGA CCC TTG GTG GGA CGT CTC ATT CAC CAG CTT CTC ACA GAC Thr Pro Arg Pro Leu Val Gly Arg Leu Ile His Gln Leu Leu Thr Asp 1950 1955 1960			5968
85	ATT GGT CGG TAC CAC CCC CAG GCC CTC ATC TAC CCA CTG ACA GTG GCT Ile Gly Arg Tyr His Pro Gln Ala Leu Ile Tyr Pro Leu Thr Val Ala 1965 1970 1975			6016
90	TCT AAG TCT ACC ACG ACA GCC CGG CAC AAT GCA AAC AAG ATT CTG			6064

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	Ser Lys Ser Thr Thr Ala Arg His Asn Ala Ala Asn Lys Ile Leu	
	1980 1985 1990 1995	
5	AAG AAC ATG TGT GAG CAC AGC AAC ACC CTG GTC CAG CAG GCC ATG ATG Lys Asn Met Cys Glu His Ser Asn Thr Leu Val Gln Gln Ala Met Met 2000 2005 2010	6112
10	GTG AGC GAG GAG CTG ATC CGA GTG GCC ATC CTC TGG CAT GAG ATG TGG Val Ser Glu Glu Leu Ile Arg Val Ala Ile Leu Trp His Glu Met Trp 2015 2020 2025	6160
15	CAT GAA GGC CTG GAA GAG GCA TCT CGT TTG TAC TTT GGG GAA AGG AAC His Glu Gly Leu Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn 2030 2035 2040	6208
20	GTG AAA GGC ATG TTT GAG GTG CTG GAG CCC TTG CAT GCT ATG ATG GAA Val Lys Gly Met Phe Glu Val Leu Glu Pro Leu His Ala Met Met Glu 2045 2050 2055	6256
25	CGG GGC CCC CAG ACT CTG AAG GAA ACA TCC TTT AAT CAG GCC TAT GGT Arg Gly Pro Gln Thr Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly 2060 2065 2070 2075	6304
30	CGA GAT TTA ATG GAG GCC CAA GAG TGG TGC AGG AAG TAC ATG AAA TCA Arg Asp Leu Met Glu Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser 2080 2085 2090	6352
35	GGG AAT GTC AAG GAC CTC ACC CAA GCC TGG GAC CTC TAT TAT CAT GTG Gly Asn Val Lys Asp Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His Val 2095 2100 2105	6400
40	TTC CGA CGA ATC TCA AAG CAG CTG CCT CAG CTC ACA TCC TTA GAG CTG Phe Arg Arg Ile Ser Lys Gln Leu Pro Gln Leu Thr Ser Leu Glu Leu 2110 2115 2120	6448
45	CAA TAT GTT TCC CCA AAA CTT CTG ATG TGC CGG GAC CTT GAA TTG GCT Gln Tyr Val Ser Pro Lys Leu Leu Met Cys Arg Asp Leu Glu Leu Ala 2125 2130 2135	6496
50	GTG CCA GGA ACA TAT GAC CCC AAC CAG CCA ATC ATT CGC ATT CAG TCC Val Pro Gly Thr Tyr Asp Pro Asn Gln Pro Ile Ile Arg Ile Gln Ser 2140 2145 2150 2155	6544
55	ATA GCA CCG TCT TTG CAA GTC ATC ACA TCC AAG CAG AGG CCC CGG AAA Ile Ala Pro Ser Leu Gln Val Ile Thr Ser Lys Gln Arg Pro Arg Lys 2160 2165 2170	6592
60	TTG ACA CTT ATG GGC AGC AAC GGA CAT GAG TTT GTT TTC CTT CTA AAA Leu Thr Leu Met Gly Ser Asn Gly His Glu Phe Val Phe Leu Leu Lys 2175 2180 2185	6640
65	GGC CAT GAA GAT CTG CGC CAG GAT GAG CGT GTG ATG CAG CTC TTC GGC Gly His Glu Asp Leu Arg Gln Asp Glu Arg Val Met Gln Leu Phe Gly 2190 2195 2200	6688
70	CTG GTT AAC ACC CTT CTG GCC AAT GAC CCA ACA TCT CTT CGG AAA AAC Leu Val Asn Thr Leu Leu Ala Asn Asp Pro Thr Ser Leu Arg Lys Asn 2205 2210 2215	6736
75	CTC ATT GGC TGG GTT CCC CAC TGT GAC ACA CTG CAC GCC CTC ATC CGG Leu Ile Gly Trp Val Pro His Cys Asp Thr Leu His Ala Leu Ile Arg 2220 2225 2230 2235	6784
80	CTC ATT GGC TGG GTT CCC CAC TGT GAC ACA CTG CAC GCC CTC ATC CGG Leu Ile Gly Trp Val Pro His Cys Asp Thr Leu His Ala Leu Ile Arg 2240 2245 2250	6832
85	GAC TAC AGG GAG AAG AAG ATC CTT CTC AAC ATC GAG CAT CGC ATC Asp Tyr Arg Glu Lys Lys Ile Leu Leu Asn Ile Glu His Arg Ile 2255 2260 2265	6880

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	ATG TTG CGG ATG GCT CCG GAC TAT GAC CAC TTG ACT CTG ATG CAG AAG Met Leu Arg Met Ala Pro Asp Tyr Asp His Leu Thr Leu Met Gln Lys 2270 2275 2280	6928
5	GTG GAG GTG TTT GAG CAT GCC GTC AAT AAT ACA GCT GGG GAC GAC CTG Val Glu Val Phe Glu His Ala Val Asn Asn Thr Ala Gly Asp Asp Leu 2285 2290 2295	6976
10	GCC AAG CTG CTG TGG CTG AAA AGC CCC AGC TCC GAG GTG TGG TTT GAC Ala Lys Leu Leu Trp Leu Lys Ser Pro Ser Ser Glu Val Trp Phe Asp 2300 2305 2310 2315	7024
15	CGA AGA ACC AAT TAT ACC CGT TCT TTA GCG GTC ATG TCA ATG GTT GGG Arg Arg Thr Asn Tyr Thr Arg Ser Leu Ala Val Met Ser Met Val Gly 2320 2325 2330	7072
20	TAT ATT TTA GGC CTG GGA GAT AGA CAC CCA TCC AAC CTG ATG CTG GAC Tyr Ile Leu Gly Leu Gly Asp Arg His Pro Ser Asn Leu Met Leu Asp 2335 2340 2345	7120
25	CGT CTG AGT GGG AAG ATC CTG CAC ATT GAC TTT GGG GAC TGC TTT GAG Arg Leu Ser Gly Lys Ile Leu His Ile Asp Phe Gly Asp Cys Phe Glu 2350 2355 2360	7168
30	GTT GCT ATG ACC CGA GAG AAG TTT CCA GAG AAG ATT CCA TTT AGA CTA Val Ala Met Thr Arg Glu Lys Phe Pro Glu Lys Ile Pro Phe Arg Leu 2365 2370 2375	7216
35	ACA AGA ATG TTG ACC AAT GCT ATG GAG GTT ACA GGC CTG GAT GGC AAC Thr Arg Met Leu Thr Asn Ala Met Glu Val Thr Gly Leu Asp Gly Asn 2380 2385 2390 2395	7264
40	TAC AGA ATC ACA TGC CAC ACA GTG ATG GAG GTG CTG CGA GAG CAC AAG Tyr Arg Ile Thr Cys His Thr Val Met Glu Val Leu Arg Glu His Lys 2400 2405 2410	7312
45	GAC AGT GTC ATG GCC GTG CTG GAA GCC TTT GTC TAT GAC CCC TTG CTG Asp Ser Val Met Ala Val Leu Glu Ala Phe Val Tyr Asp Pro Leu Leu 2415 2420 2425	7360
50	AAC TGG AGG CTG ATG GAC ACA AAT ACC AAA GGC AAC AAG CGA TCC CGA Asn Trp Arg Leu Met Asp Thr Asn Thr Lys Gly Asn Lys Arg Ser Arg 2430 2435 2440	7408
55	ACG AGG ACG GAT TCC TAC TCT GCT GGC CAG TCA GTC GAA ATT TTG GAC Thr Arg Thr Asp Ser Tyr Ser Ala Gly Gln Ser Val Glu Ile Leu Asp 2445 2450 2455	7456
60	GGT GTG GAA CTT GGA GAG CCA GCC CAT AAG AAA ACG GGG ACC ACA GTG Gly Val Glu Leu Gly Glu Pro Ala His Lys Lys Thr Gly Thr Thr Val 2460 2465 2470 2475	7504
65	CCA GAA TCT ATT CAT TCT TTC ATT GGA GAC GGT TTG GTG AAA CCA GAG Pro Glu Ser Ile His Ser Phe Ile Gly Asp Gly Leu Val Lys Pro Glu 2480 2485 2490	7552
70	GCC CTA AAT AAG AAA GCT ATC CAG ATT ATT AAC AGG GTT CGA GAT AAG Ala Leu Asn Lys Ala Ile Gln Ile Ile Asn Arg Val Arg Asp Lys 2495 2500 2505	7600
	CTC ACT GGT CGG GAC TTC TCT CAT GAT GAC ACT TTG GAT GTT CCA ACG Leu Thr Gly Arg Asp Phe Ser His Asp Asp Thr Leu Asp Val Pro Thr 2510 2515 2520	7648
	CAA GTT GAG CTG CTC ATC AAA CAA GCG ACA TCC CAT GAA AAC CTC TGC Gln Val Glu Leu Leu Ile Lys Gln Ala Thr Ser His Glu Asn Leu Cys 2525 2530 2535	7696
	CAG TGC TAT ATT GGC TGG TGC CCT TTC TGG TAACTGGAGG CCCAGATGTG Gln Cys Tyr Ile Gly Trp Cys Pro Phe Trp 2540 2545	7746

CCCATCACGT TTTTTCTGAG GCTTTGTAC TTTAGTAAAT GCTTCCACTA AACTGAAACC 7806
 5 ATGGTGAGAA AGTTTGACTT TGTTAAATAT TTTGAAATGT AAATGAAAAG AAGTACTGTA 7866
 TATTAAAAGT TGGTTTGAAC CAACTTTCTA GCTGCTGTTG AAGAATATAT TGTCAGAAC 7926
 .ACAAGGCTTG ATTTGGT 7943

10 (2) INFORMATION FOR SEQ ID NO:3:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 723 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA

25 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 15..509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

30	GTGTACTATT AGCC ATG GTC AAC CCC ACC GTG TTC TTC GAC ATT GCC GTC Met Val Asn Pro Thr Val Phe Phe Asp Ile Ala Val 1 5 10	50
35	GAC GGC GAG CCC TTG GGC CGC GTC TCC TTT GAG CTG TTT GCA GAC AAG Asp Gly Glu Pro Leu Gly Arg Val Ser Phe Glu Leu Phe Ala Asp Lys 15 20 25	98
40	GTC CCA AAG ACA GCA GAA AAT TTT CGT GCT CTG AGC ACT GGA GAG AAA Val Pro Lys Thr Ala Glu Asn Phe Arg Ala Leu Ser Thr Gly Glu Lys 30 35 40	146
45	GGA TTT GGT TAT AAG GGT TCC TGC TTT CAC AGA ATT ATT CCA GGG TTT Gly Phe Gly Tyr Lys Gly Ser Cys Phe His Arg Ile Ile Pro Gly Phe 45 50 55 60	194
50	ATG TGT CAG GGT GGT GAC TTC ACA CGC CAT AAT GGC ACT GGT GGC AAG Met Cys Gln Gly Asp Phe Thr Arg His Asn Gly Thr Gly Lys 65 70 75	242
55	TCC ATC TAT GGG GAG AAA TTT GAA GAT GAG AAC TTC ATC CTA AAG CAT Ser Ile Tyr Gly Glu Lys Phe Glu Asp Glu Asn Phe Ile Leu Lys His 80 85 90	290
60	ACG GGT CCT GGC ATC TTG TCC ATG GCA AAT GCT GGA CCC AAC ACA AAT Thr Gly Pro Gly Ile Leu Ser Met Ala Asn Ala Gly Pro Asn Thr Asn 95 100 105	338
65	GGT TCC CAG TTT TTC ATC TGC ACT GCC AAG ACT GAG TGG TTG GAT GGC Gly Ser Gln Phe Phe Ile Cys Thr Ala Lys Thr Glu Trp Leu Asp Gly 110 115 120	386
70	AAG CAT GTG GTG TTT GGC AAA GTG AAA GAA GGC ATG AAT ATT GTG GAG Lys His Val Val Phe Gly Lys Val Lys Glu Gly Met Asn Ile Val Glu 125 130 135 140	434
75	GCC ATG GAG CGC TTT GGG TCC AGG AAT GGC AAG ACC AGC AAG AAG ATC Ala Met Glu Arg Phe Gly Ser Arg Asn Gly Lys Thr Ser Lys Lys Ile 145 150 155	482
80	ACC ATT GCT GAC TGT GGA CAA CTC GAA TAAGTTGAC TTGTGTTTA Thr Ile Ala Asp Cys Gly Gln Leu Glu 160 165	529

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TCTTAACCAC CAGATCATT	TCAGGAGAGC ACCCCTCCAC CCCATTGCT	589
CGCAGTATCC TAGAATCTTT GTGCTCTCGC TGCAGTTCCC TTTGGGTTCC ATGTTTCCT	649	
5 TGTTCCCTCC CATGCCTAGC TGGATTGCAG AGTTAAGTTT ATGATTATGA AATAAAACT	709	
AAATAACAAT TGTC	723	

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